



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 142220

To: Nita M Minnifield
Location: rem/3c01/3c18
Art Unit: 1645
Monday, January 24, 2005

Case Serial Number: 09/837344

From: Beverly Shears
Location: Remsen Bldg.
RM 1A54
Phone: 571-272-2528

beverly.shears@uspto.gov

Search Notes

Reviewed
2-1-05
MM.

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 20:53:48 ; Search time 4375 seconds

(without alignments) 16019.048 Million cell updates/sec

Title: US-09-837-344-41

Perfect score: 1482

Sequence: 1 CAAGAACACAAAGCCTCT.....AAATTTTATGAACTTATAA 1482

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched:

4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBank:*

1: gb_ba:*

2: gb_htg:*

3: gb_in:*

4: gb_cm:*

5: gb_ov:*

6: gb_pat:*

7: gb_ph:*

8: gb_pl:*

9: gb_pr:*

10: gb_ro:*

11: gb_sts:*

12: gb_sy:*

13: gb_un:*

14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB	ID	Description
1	1482	100.0	1482	6	AR162970 Sequence
2	1482	100.0	1482	6	AR178259 Sequence
3	1482	100.0	1482	3	PFPLS13
4	1480.4	99.9	1482	6	AR162974 Sequence
5	1480.4	99.9	1482	6	AR178263 Sequence
6	1446	97.6	1493	6	AR28743 cDNA for LS
7	1446	97.6	1493	6	AR152957 Sequence
8	1446	97.6	1493	6	AR178256 Sequence
9	1442	97.3	5970	3	PFPLS14
10	1406.8	94.9	253001	3	AE014834
11	950	64.1	950	6	AR28740 cDNA for LS
12	950	64.1	950	6	AR162961 Sequence
13	64.1	950	6	AR178250 Sequence	
14	843	56.9	843	3	PFPLS1C
15	841.4	56.8	843	3	PFPLS1B
16	841.4	56.8	843	3	PFPLS1H
17	841.4	56.8	843	3	PFPLS1J
18	841.4	56.8	843	3	PFPLS1L
19	839.8	56.7	839.8	3	PFPLS1T

ALIGNMENTS

20	839.8	56.7	843	3	PFPLS1F	140888 Plasmid
21	839.8	56.7	843	3	PFPLS1K	140893 Plasmid
22	839.8	56.7	843	3	PFPLS1L	140834 Plasmid
23	838.2	56.6	843	3	PFPLS1M	140835 Plasmid
24	836.6	56.5	843	3	PFPLS1N	140947 Plasmid
25	836.6	56.5	843	3	PFPLS1D	140886 Plasmid
26	836.6	56.5	843	3	PFPLS1O	140836 Plasmid
27	835.6	56.5	843	3	PFPLS1G	140837 Plasmid
28	835	56.3	843	3	PFPLS1C	140910 Plasmid
29	835	56.3	843	3	PFPLS1J	140892 Plasmid
30	833.4	56.2	843	3	PFPLS1A	140908 Plasmid
31	833.4	56.2	843	3	PFPLS1B	140909 Plasmid
32	791.8	53.4	795	3	AF046996	AF046996 Plasmid
33	472.8	31.9	988	3	PFPLS15	Z30319 P. falciparu
34	472.8	31.9	988	6	A28742	A28742 cDNA for LS
35	472.8	31.9	988	6	AR162963	AR162963 Sequence
36	472.8	31.9	988	6	AR178252	Sequence
37	470.8	31.8	954	6	AR162966	AR162966 Sequence
38	470.8	31.8	954	6	AR178255	AR178255 Sequence
39	274.4	18.5	208332	10	AC122227	Mus muscu
40	252.4	17.0	172716	2	AC15383	Rattus no
41	250.8	16.9	184015	10	AC144849	Mus muscu
42	242.6	16.4	208485	2	AC149597	Mus muscu
43	225.8	15.2	2069	6	E10125	E10125 DNA encodin
44	225.8	15.2	3399	6	E10126	Continuation (2 of
45	215.8	14.6	110000	2	AC12938_1	

ORIGIN

RESULT 1	AR162970	AR162970	AR162970	1482 bp	DNA	linear	PAT 17-OCT-2001
LOCUS		Sequence	41	from patent	US 6270771.		
DEFINITION							
ACCESSION		AR162970	AR162970.1	GI:16233435			
VERSION							
KEYWORDS							
SOURCE		Unknown.					
ORGANISM		Unclassified.					
REFERENCE	1 (bases 1 to 1482)						
AUTHORS	Guérin-Marchand,C. and Druilhe,P.						
TITLE	Peptide sequences specific for the hepatic stages of <i>P. falciparum</i> bearing epitopes capable of stimulating the T lymphocytes						
JOURNAL	Patent: US 6270771-A 41-07-AUG-2001;						
FEATURES	Location/Qualifiers						
	1. 1-1482						
	/mol_type="unassigned DNA"						

ORIGIN

Query	Match	Best Local Similarity	100.0%	Score	1482	DB	6	Length	1482
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Qy	1	CAAGAACACAAAGCGCTAGACAGAGACGCGCTTAAGAAAGTGTGCAAGACAA	60						
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Qy	61	CAACCGATTAGACAGATAGACTCTAAAGAAAGTGTGCAAGACAAACCGATCTGAA	120						
Db	61	CAACCGATTAGACAGATAGACTCTAAAGAAAGTGTGCAAGACAAACCGATCTGAA	120						
Qy	121	TAGAACAGAGAGACTCTAAAGAAAGTGTGCAAGACAAACCGATCTGAA	180						
Db	121	TAGAACAGAGAGACTCTAAAGAAAGTGTGCAAGACAAACCGATCTGAA	180						
Qy	181	GAGAAGCTGCTAAGAAAGTGTGCAAGACAAACCGATCTGAA	240						
Db	181	GAGAAGCTGCTAAGAAAGTGTGCAAGACAAACCGATCTGAA	240						

L40885 Plasmidium
L40884 Plasmidium
L40889 Plasmidium
L40890 Plasmidium
L40891 Plasmidium
L40887 Plasmidium

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Om nucleic - nucleic search, using SW model

Run on: January 22, 2005, 20:50:38 ; Search time 533 Seconds

(without alignments)
14595.951 Million cell updates/sec

Title: score: US-09-837-344-41

Perfect score: 1482

Sequence: 1 CAAGACAAACAAGCGATCT.....AATATTATGAACTATA 1482

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2634710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_23Sep04:*

1: geneseqn1988:*2: geneseqn1998:*3: geneseqn2000s:*4: geneseqn2001as:*5: geneseqn2001bs:*6: geneseqn2002as:*7: geneseqn2002bs:*8: geneseqn2003as:*9: geneseqn2003bs:*10: geneseqn2003s:*11: geneseqn2003db:*12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

repeat_region

repeat_unit

/tag= a

37. .87

/tag= b

/rpt_type= TANDEM

DN WO2013884-A1.

XX PD 20-AUG-1992.

XX PP 05-FEB-1992; 92WO-FR000104.

XX PR 05-FEB-1991; 91FR-00001286.

XX P-PSDB; AAR26944.

XX PT Polypeptide(s) derived from liver stage of PLASMODIUM FALCIPARUM - for vaccination against, treatment of and diagnosis of malaria.

22 136.4 9.2 7797 2 AX33180 Ax33180 Copepox vi 23 135.4 9.2 7996 2 AX33184 Bae sequ 24 132.8 9.0 778 6 ABQ15588 Abq15588 Oligonucl 25 132.8 9.0 778 6 ABQ15589 Abq15589 Oligonucl 26 131.4 8.9 7442 4 AS46606 Tumour su 27 129.8 8.8 1762 6 ABQ20939 Abq20939 Oligonucl 28 129.8 8.8 1762 6 ABQ20938 Abq20938 Oligonucl 29 129.2 8.7 1995 6 ABQ20942 Abq20942 Oligonucl 30 129.2 8.7 1995 6 ABQ20943 Abq20943 Oligonucl 31 129 8.7 1200 6 ABQ39210 Abq39210 Oligonucl 32 129 8.7 1200 6 ABQ39211 Abq39211 Oligonucl 33 129 8.7 7597 6 ABQ33953 Abq33953 Human imm 34 129 8.7 1006 6 ABQ33958 Abq33958 Human imm 35 127.4 8.6 3683 8 ABQ10053 Abq10053 Haematoopo 36 127 8.6 3683 8 ABQ10053 Abq10053 Haematoopo 37 123.4 8.3 3037 6 ABQ54065 Abq54065 Oligonucl 38 123.4 8.3 3037 6 ABQ54067 Abq54067 Oligonucl 39 123 8.3 12237 6 ABQ34358 Abq34358 Human imm 40 120.4 8.1 1533 8 ACB28672 ACB28672 Prokaryot 41 120.4 8.1 6419 6 ABQ32671 Human imm 42 118.6 8.0 975 6 ABQ29508 Abq29508 Oligonucl 43 118.6 8.0 975 6 ABQ29509 Abq29509 Oligonucl 44 118.6 8.0 975 6 ABQ33103 Human imm 45 117.8 7.9 6898 6 ABN80222 Abn80222 Human cne

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Om nucleic - nucleic search, using sw model

Run on: January 22, 2005, 23:08:59 ; Search time 101 seconds

Perfect score: 1482 ; (without alignments) 10429.595 Million cell updates/sec

Title: US-09-837-344-41
 Sequence: 1 CAAGACAAACAAAGCGACT.....AATATTATGAAACTATA 1482
 Scoring table: IDENTITY_NUC
 Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 35539441 residues

Total number of hits satisfying chosen parameters: 1649014
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% ; Maximum Match 100% ; Listing first 45 summaries

Database : Issued_Patents_NA:*

- 1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
- 2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
- 3: /cgn2_5/ptodata/1/ina/6A_COMB.seq:*
- 4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
- 5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
- 6: /cgn2_6/ptodata/1/ina/backFiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	1482	100.0	1482	3	US-09-098-3273-41		Sequence 41, Appl
2	1482	100.0	1482	3	US-09-462-625-41		Sequence 41, Appl
3	1480.4	99.9	1482	3	US-09-098-3273-45		Sequence 45, Appl
4	1480.4	99.9	1482	3	US-09-462-625-45		Sequence 45, Appl
5	1446	97.6	1493	3	US-09-098-3273-38		Sequence 38, Appl
6	950	64.1	950	3	US-09-098-3273-32		Sequence 32, Appl
7	950	64.1	950	3	US-09-462-625-32		Sequence 32, Appl
8	853.2	57.6	1320	1	US-09-462-625-15		Sequence 15, Appl
9	853.2	57.6	1320	1	US-09-462-625-15		Sequence 15, Appl
10	472.8	31.9	988	3	US-09-098-3273-34		Sequence 34, Appl
11	472.8	31.9	988	3	US-09-462-625-34		Sequence 34, Appl
12	470.8	31.8	954	3	US-09-098-3273-37		Sequence 37, Appl
13	470.8	31.8	954	3	US-09-462-625-37		Sequence 37, Appl
14	116.2	7.8	3095	6	5231168-1		Patent No. 5231168
15	111.6	7.5	1827	4	US-09-270-767-1308		Sequence 1308, Appl
16	111.6	7.4	7218	1	US-09-232-463-14		Sequence 16590, Appl
17	101.2	6.8	3	US-09-552-8461-1		Sequence 34, Appl	
18	101.2	6.8	1956	4	US-09-351-7948-1		Sequence 37, Appl
19	101.2	6.8	1956	4	US-09-973-462-2		Sequence 37, Appl
20	93.6	6.3	5361	3	US-09-973-462-2		Sequence 37, Appl
21	93.6	6.3	5361	3	US-09-973-462-1		Sequence 37, Appl
22	89.6	6.0	164976	4	US-09-916-421B-1		Sequence 1, Appl
23	89.6	6.0	164976	4	US-09-622-570-1		Sequence 1, Appl
24	88.4	6.0	5340	4	US-09-627-122-21		Sequence 21, Appl
25	87	5.9	699	4	US-09-248-7964-9722		Sequence 9722, Appl
26	86.8	5.9	4766	5	PCT-US93-07261-10		Sequence 10, Appl
27	83.2	5.6	1669	3	US-09-461-697-184		Sequence 184, Appl

ALIGNMENTS

RESULT 1
 US-09-098-3273-41
 ; Sequence 41, Appl
 ; Patent No. 620771
 ; GENERAL INFORMATION:
 ; APPLICANT: GUEBIN-MARCHAND, Claudine
 ; APPLICANT: DRUILHE, Pierre
 ; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE T LYMPHOCYTES
 ; TITLE OF INVENTION: OF STIMULATING THE T LYMPHOCYTES
 ; NUMBER OF SEQUENCES: 46
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Burn, Doane, Swecker & Mathis
 ; STREET: P.O. Box 1404
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States
 ; ZIP: 22313-1404
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-POS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US-09-098-3273-41
 ; FILING DATE: 24-NOV-1993
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: FR 91 01286
 ; FILING DATE: 05-FEB-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: McCowan, Malcolm K.
 ; NAME: McCowan, Malcolm K.
 ; REGISTRATION NUMBER: 39,300
 ; REFERENCE/DOCKET NUMBER: 010830-0445
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-6620
 ; TELEFAX: (703) 836-2021
 ; INFORMATION FOR SEQ ID NO: 41:
 ; SEQENCE CHARACTERISTICS:
 ; LENGTH: 1482 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (Genomic)
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1482
 ; PUBLICATON INFORMATION:
 ; DOCUMENT NUMBER: WO 92/13884
 ; PUBLICATION DATE: 20-AUG-1992

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Om nucleic - nucleic search, using SW model

Run on: January 23, 2005, 00:49:49 ; Search time 611 seconds

(without alignments) 13936.833 Million cell updates/sec

Title: US-09-837-344-41

Perfect score: 1482

Sequence: 1 CAAAGACAAACAAAGCGATCT.....AATATTATGAAACTATAA 1482

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4300275 seqs, 2872944193 residue

Total number of hits satisfying chosen parameters: 8600550

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications NA.*

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2: /cgn2_6/ptodata/1/pubpna/us08_pubcomb.seq;*

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4: /cgn2_6/ptodata/1/pubpna/us06_pubcomb.seq;*

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21: /cgn2_6/ptodata/1/pubpna/us60_pubcomb.seq;*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1482	100.0	1482	Sequence 41, Appl
2	1482	100.0	1482	Sequence 41, Appl
3	1480	99.9	1482	Sequence 41, Appl
4	1480	99.9	1482	Sequence 41, Appl
5	1466	97.6	1493	Sequence 45, Appl
6	1446	97.6	1493	Sequence 38, Appl
7	950	64.1	950	Sequence 38, Appl
8	950	64.1	10	Sequence 32, Appl
9	472.8	31.9	988	Sequence 32, Appl
10	472.8	31.9	988	Sequence 34, Appl
11	470.8	31.8	954	Sequence 34, Appl
12	470.8	31.8	954	Sequence 37, Appl
13	470.8	31.8	954	Sequence 37, Appl

RESULT 1
US-09-837-344-41
; Sequence 41, Application US/09837344
; Patent No. US2002041882A1
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; DRUILHE, Pierre
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; HEPATIC STAGES OF P. FALCIPARUM BEARING EPITOPES CAPABLE
; OF STIMULATING THE T LYMPHOCYTES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404

ALIGNMENTS

13	233.4	15.7	1300	17	US-10-668-749A-1	Sequence 1, Appl
14	153.2	10.3	1297	18	US-10-425-115-6787	Sequence 6756, A
15	151.2	10.2	6292	16	US-10-221-714A-661	Sequence 461, APP
16	149.2	10.1	6767	16	US-10-221-714A-330	Sequence 330, APP
17	145.8	9.8	1243	17	US-10-425-115-72717	Sequence 172717, A
18	145	9.8	1204	17	US-10-437-963-77858	Sequence 77858, A
19	142.4	9.6	1081	18	US-10-425-115-16756	Sequence 16756, A
20	139.4	9.4	9539	14	US-10-239-676-52	Sequence 52, APP
21	135.4	9.4	9539	15	US-10-240-453-54	Sequence 54, APP
22	137.8	9.3	6668	15	US-10-311-455-1610	Sequence 1670, AP
23	132.8	9.0	778	18	US-10-363-345A-2180	Sequence 1719, AP
24	132.8	9.0	778	18	US-10-363-345A-7533	Sequence 1729, AP
25	131.4	8.9	7442	16	US-10-221-714A-409	Sequence 2180, AP
26	129.8	8.8	1821	18	US-10-425-115-38210	Sequence 409, APP
27	129.8	8.8	1762	18	US-10-363-345A-7529	Sequence 986, APP
28	129.8	8.8	1762	18	US-10-363-345A-7530	Sequence 1986, APP
29	129.2	8.7	1995	18	US-10-363-345A-7533	Sequence 1931, AP
30	129.2	8.7	1995	18	US-10-363-345A-7534	Sequence 1533, AP
31	129	8.7	1200	18	US-10-363-345A-25802	Sequence 1534, AP
32	129	8.7	1200	18	US-10-363-345A-25802	Sequence 25801, A
33	129	8.7	7597	15	US-10-311-455-986	Sequence 25802, A
34	129	8.7	1406	15	US-10-311-55-1931	Sequence 986, APP
35	128.6	8.7	367778	15	US-10-312-841-1	Sequence 1931, AP
36	128.6	8.7	367778	15	US-10-425-115-120013	Sequence 1931, AP
37	127.4	8.6	3683	18	US-10-473-126-339	Sequence 2, APP
38	127	8.6	3683	18	US-10-425-115-132399	Sequence 339, APP
39	127	8.6	3683	18	US-10-473-126-193	Sequence 193, APP
40	126.2	8.5	880	18	US-10-425-115-53133	Sequence 53133, A
41	126.2	8.4	986	18	US-10-425-115-17478	Sequence 17478, A
42	123.8	8.4	1062	18	US-10-425-115-120013	Sequence 120013, A
43	123.4	8.3	3037	18	US-10-363-345A-0657	Sequence 40657, A
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45	123	8.3	12237	15	US-10-311-455-2331	Sequence 2331, AP

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09837344
FILING DATE: 15-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/462,625
FILING DATE: <Unknown>
APPLICATION NUMBER: FR 91 01286
FILING DATE: 05-FEB-1991
ATTORNEY/AGENT INFORMATION:
NAME: McGowan, Malcolm K.
REGISTRATION NUMBER: 39,300

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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: January 22, 2005, 23:02:29 ; Search time 3390 Seconds

15930.290 Million cell updates/sec

Title: US-09-837-344-41
Perfect score: 1482
Sequence: CAAGAACACAAAGCCATCT.....ATATTTTATGAACTATAA 1482

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 33822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*

2: gb_est2:*

3: gb_htc:*

4: gb_est3:*

5: gb_est4:*

6: gb_est5:*

7: gb_est6:*

8: gb_gss1:*

9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID

Description

RESULT 1

T09652

T09652

T09652

T09652.1

GI:319484

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Other_GSS: 0224m7

Contact: Dame JB

Dept. of Pathobiology, College of Veterinary Medicine

University of Florida

2015 SW 33rd Avenue, Bldg 1017, Gainesville, FL 32611, USA

Tel: 352 392 4700

Fax: 352 3974

Email: damej@mail.vetmed.ufl.edu

Seq primer: T3

Class: shotgun

Location/Qualifiers

FEATURES

source

1. .317

/organism="Plasmodium falciparum"

/mol_type="genomic DNA"

/db_xref="Taxon:5833"

/clone="0224m7"

/lab_host="E. coli XLI-Blue"

/clone_id="gbpPFH3.1", G. Roman Reddy"

/note="Vector: pBlueScript SK(+); Genomic DNA, from asynchronous blood stage parasites; of the cloned Honduran

HB3 isolate cultured in vitro, was digested with mung bean

nuclease in the presence of 30% formamide at 50°C (Vernick, K.D., Imberski, R.B., and McCutchan, T.P. 1988.

Nucleic Acids Research 16:6883-6996). The ends of the

fragments were polished using T4 DNA polymerase, and the

fragments were ligated to ECR V-cleaved and

dephosphorylated pBlueScript SK(+). Recombinant plasmids

transformed E. coli XLI-Blue."

ALIGNMENTS

c 25 228 8 15.4 1566 9 CG757757
c 26 228 6 15.4 1434 8 CC187638
c 27 228 4 15.4 1507 9 CC187639
c 28 228 4 15.4 1823 9 AG346189
c 29 228 4 15.4 1259 9 CL058635
c 30 228 15.4 2033 9 CR04722
c 31 228 15.4 2103 9 CL041093
c 32 227.6 15.4 1712 9 CL078539
c 33 226.8 15.3 1547 9 CL066420
c 34 226.6 15.3 1377 9 CL077307
c 35 226.4 15.3 1716 8 CC222065
c 36 225.6 15.2 1562 9 CL078533
c 37 225.6 15.2 1651 9 CL079030
c 38 225.4 15.2 1482 9 AG332292
c 39 224.2 15.1 1506 9 CL082761
c 40 224 15.1 1336 9 CL078538
c 41 224 15.1 1289 9 CL082577
c 42 223.8 15.1 2001 9 CL118787
c 43 223.6 15.1 1394 9 CL078613
c 44 223.6 15.1 1757 9 CL078645
c 45 223.4 15.1 1680 9 CL079033

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Om nucleic - protein search, using frame_plus_n2p model

Run on: January 14, 2005, 20:38:17 ; Search time 44 Seconds

(without alignments) 4467.422 Million cell updates/sec

Title: US-09-837-344-41
Perfect score: 2486

Sequence: 1 CAAGACAAACAAAGGGACT.....AATATTATGAACTATA 1482

Scoring table: BLOSUM62

Xgapop 1.0.0 , Xgapext 0.5

Ygapop 1.0.0 , Ygapext 0.5

Fgapop 6.0 , Fgapext 7.0

Delect 6.0 , Delect 7.0

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 956278

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Command line parameters:

```
-MODE=frame+n2p.model -DEV=xlp
-O=/cgn2_1/USPTO/spool_p/US09837344/runat_14012005_143843_4437/app_query.fasta_1.1671
-DB=Issued Patents AA -ORM=FastaN -SUFFIX=rai -MINMATCH=0.1 -LOCAL=0
-LOCPAT=0 -UNITS=Bits -START=1 -END=-1 -THR=MAX=100 -THR_MIN=0 -ALIGN=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -MAXLEN=2000000000
-MODE=LOCAL -OUTMFT=pct -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-NO_MMW -LARGEQUERY -NBB_SCORES=0 -WAIT=1 -DSPBLOCK=700 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPEXT=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DBOPEN=6 -DELEXT=7
```

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5a_comb.pep:*
- 2: /cgn2_6/ptodata/1/iaa/5b_comb.pep:*
- 3: /cgn2_6/ptodata/1/iaa/6a_comb.pep:*
- 4: /cgn2_6/ptodata/1/iaa/6b_comb.pep:*
- 5: /cgn2_6/ptodata/1/iaa/PC15_Comb.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1549	62.3	316	US-09-098-3278-31
2	1549	62.3	316	US-08-462-621-31
3	603	24.3	3	US-08-462-621-31
4	603	24.3	117	3 US-08-462-625-20
5	554	22.3	107	3 US-08-098-3278-19
6	554	22.3	107	3 US-08-462-625-19
7	376	15.1	198	1 US-08-056-200-94
8	376	15.1	189	2 US-08-800-644-94
9	376	15.1	189	4 US-09-530-1280
10	359	14.4	1162	2 US-08-720-323A-2
11	359	14.4	1162	3 US-09-290-568-2
12	359	14.4	1162	4 US-09-410-399-2

RESULT 1
US-09-837-344-41
; Sequence 31, Application US/08098327E
; Patent No. 6220771
; GENERAL INFORMATION:
; APPLICANT: GUERIN-MARCHAND, Claudine
; APPLICANT: DRUILHE, Pierre
; TITLE OF INVENTION: PEPTIDE SEQUENCES SPECIFIC FOR THE
; TITLE OF INVENTION: HEPATIC STAGES OF P. PARICIPARUM BEARING EPITOPE CAPABLE
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSE: Burns, Doane, Swecker & Mathis
; STREET: P.O. Box 1404
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States
; ZIP: 22313-1404
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/098-3278E
; FILING DATE: 24-Nov-1993
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: FR 91 01286
; FILING DATE: 05-FEB-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: McGowan, Malcolm K.
; REGISTRATION NUMBER: 39,300
; REFERENCE/DOCKET NUMBER: 010830-045
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 838-6620

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On nucleic - protein search, using frame_plus_n2p model

Run on:

January 14, 2005, 20:37:21 ; Search time 59.5 Seconds

(without alignments) 4793.050 Million cell. updates/sec

Title: US-09-837-344-41

Perfect score: 2486

Sequence: 1 CAAGAGCAACAAAGGGACTC.....AAATATTGAACTATAA 1482

Scoring table:

BLOSUM2

xgapop 10.0 , xgapext 0.5
ygapop 10.0 , ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-NODEBL=frame+ n2p.model -DEV=xlp
-DB=CGN2_79 -QFMT=fastan -SUFFIX=txt -MINMATCH=0.1 -LOOPCFL=0 -LOOPEXT=0
-UNITS=512 -START=1 -END=-1 -MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-DOCALLIG=200 -THR SCORE=PCT -THR MAX=100 -TRANS=human0.cgi -LIST=45
-OUTFMT=pto -NORMEXT -HEAITSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=USP09837344 @CGN 1 180 @runat 14012005 143842 4425 -NCPU=6 -ICPU=3
-NO MMAP -LARGEST -HEG SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7 -

Database : PIR_79;*

1: pir;*
2: pir;*
3: pir;*
4: pir;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2406.5	96.8	1909	2 A45592
2	380.5	15.3	1407	1 S28599
3	380.5	15.3	1549	1 A40691
4	376	15.1	1898	1 A45973
5	356	14.3	1017	2 T15598
6	353.5	14.2	737	2 T15597
7	332.5	13.4	1192	2 A71623
8	326.5	13.1	1979	1 S03165
9	323.5	13.0	1039	2 S18199
10	321	12.9	771	1 A33430
11	319	12.8	1938	2 JC5421
12	319	12.8	1972	2 JC5420
13	318.5	12.8	1961	1 A61231
14	317.5	12.8	1166	2 H86341

RESULT 1
A45592
Liver stage antigen ICA-1 - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;CreateDate: 22-Nov-1993 #Sequence revision 02-Dec-1994 #text change 09-Jul-2004
C;Accession: S24592; S28393; S34842; B45592; C45592; D45592
R;Zhu, J.; Hollingdale, M.
Submitted to the EMBL Data Library, November 1990
A;Reference number: S24597
A;Accession: S24597
A;Molecule type: DNA
A;Cross-references: UNIPROT:Q25893; EMBL:X56203; NID:99915; PID:99916
R;Zhu, J.; Hollingdale, M.R.
Mol. Biochem. Parasitol. 48, 223-226, 1991
A;Title: Structure of Plasmodium falciparum liver stage antigen-1.
A;Reference number: A45592; MUID:92107224; PMID:184628
A;Accession: A45592
A;Molecule type: DNA
A;Residues: 1-195-638-688-1165-1215-1590-1909 <ZH2>
A;Note: sequence extracted from NCBI backbone (NCBIN:75010, NCBIN:5012, NCBIN:75014, R;Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Patarapotikul, J.; Beaudoin, Nature 329, 164-167, 1987
A;Title: A liver-stage antigen-specific antigen of Plasmodium falciparum characterized by gen
A;Accession: S29393
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 323-387 <GU1>
A;Cross-references: EMBL:MF8266
R;Guerin-Marchand, C.; Druilhe, P.; Galey, B.; Londono, A.; Patarapotikul, J.; Beaudoin, submitted to the EMBL Data Library, April 1992
A;Description: a liver-stage-specific antigen of plasmodium falciparum characterized
A;Reference number: S34842
A;Accession: S34842
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 323-381, HKAI' <GU2>

